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12,336 genes profiled, rat cDNA library

Signal-background ratio >2.5
Percentage of the well formed spot >40%
(12,320 genes)

Filter by Fold change of 1.7 in HF- S rats (86 Genes)

Statistical analysis after log transformation (83 Genes)

Macroarrays (75 Genes)

Filter EST'S (70 Genes)

Filter repetitions (49 Genes)

FIG. 1

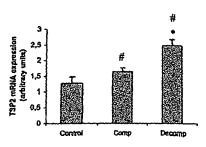


FIG. 2A

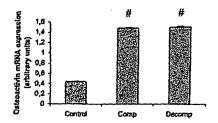


FIG. 2B

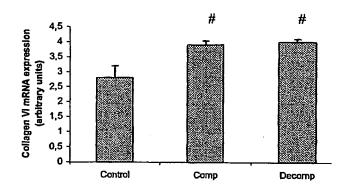


FIG. 2C

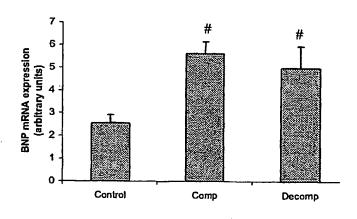


FIG. 2D

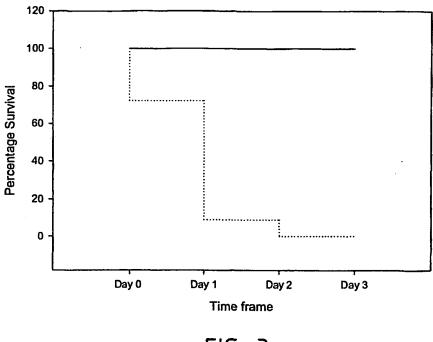


FIG. 3

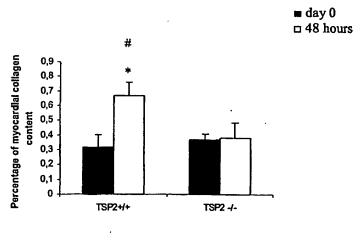


FIG. 4

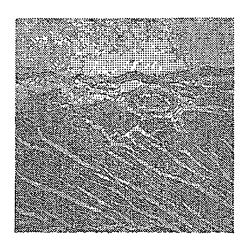


FIG. 5A

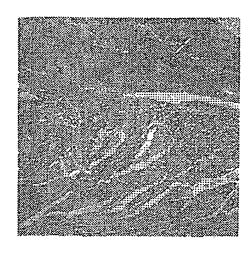


FIG. 5B

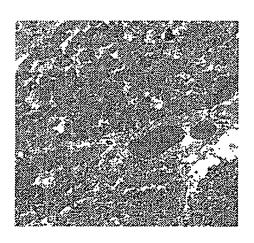


FIG. 5C

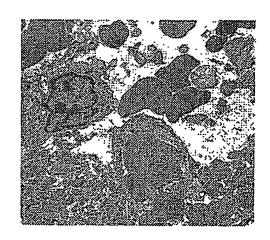
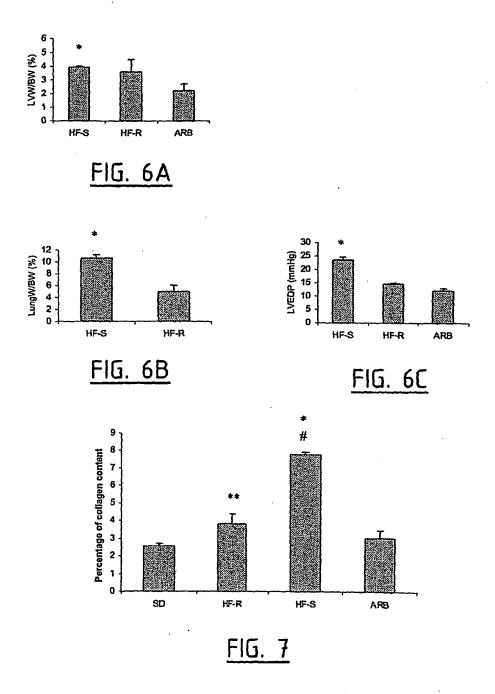


FIG. 5D



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HF-S HF-R ARB

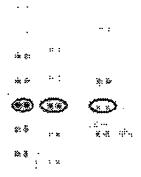
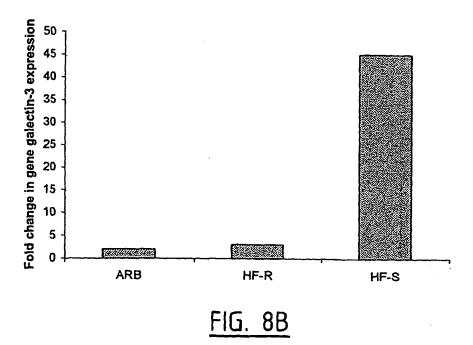


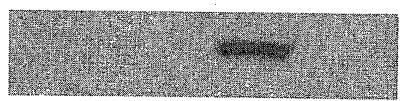
FIG. 8A





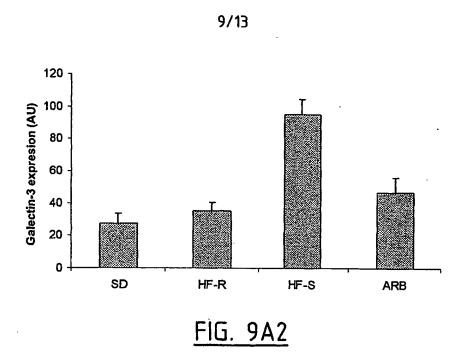
# SD HF-R HF-S ARB

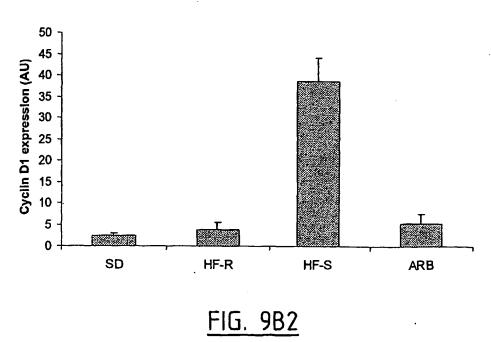
FIG. 9A1



SD HF-R HF-S ARB

FIG. 9B1





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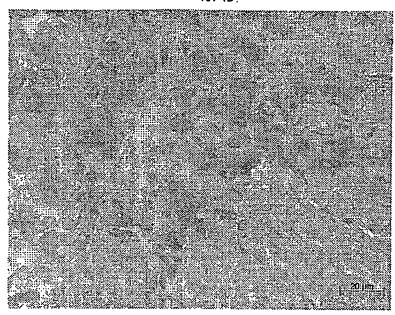


FIG. 10A

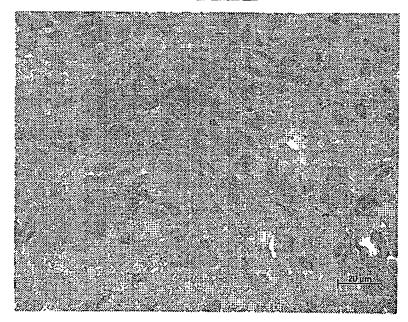


FIG. 10B

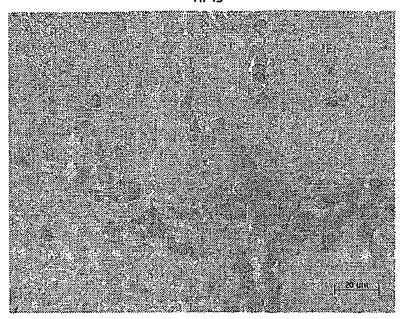


FIG. 10C

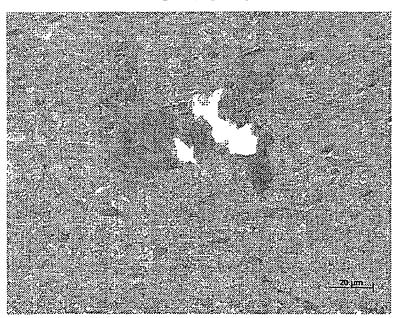


FIG. 10D

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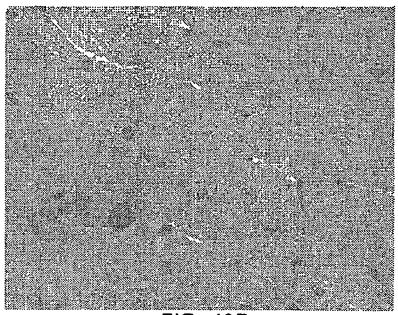


FIG. 10E

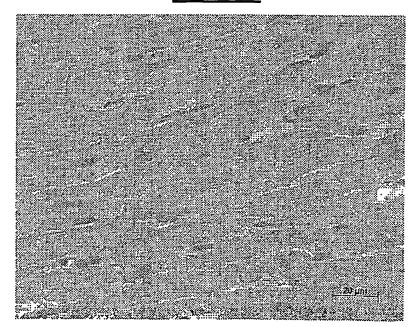
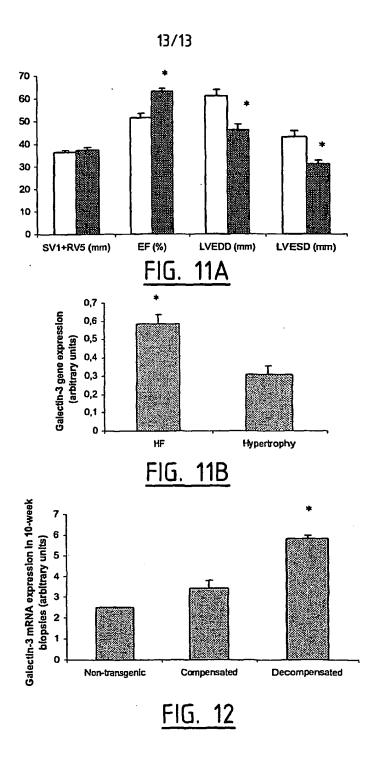


FIG. 10F



**RECTIFIED SHEET (RULE 91)** 

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